

SEQUENCE LISTING

<110> Lok, Si
Holloway, James L.

<120> Human V2 Vomeronasal Receptor

<130> 00-107

<150> 60/252,373

<151> 2000-11-21

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 657

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(657)

<400> 1

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1 5 10 15

ttt ctt gca ttt tta tgg gct gaa ttg ggc tct gaa gcc aaa gaa gag 96
Phe Leu Ala Phe Leu Trp Ala Glu Leu Gly Ser Glu Ala Lys Glu Glu
20 25 30

aaa gaa gaa gaa cgg acc tgc cgg ttg ctg ggc aag tgt gta gat gcc 144
Lys Glu Glu Glu Arg Thr Cys Arg Leu Leu Gly Lys Cys Val Asp Ala
35 40 45

gaa aac cat tcc ctt gtt att gga gga ctg ttt cct att gac tcc agg 192
Glu Asn His Ser Leu Val Ile Gly Gly Leu Phe Pro Ile Asp Ser Arg
50 55 60

acc atc cca gca aat gag tct att ttg gag cca gca tca gca aaa tgt 240
 Thr Ile Pro Ala Asn Glu Ser Ile Leu Glu Pro Ala Ser Ala Lys Cys
 65 70 75 80

gaa ggg ttt aac ttt cag aga ttc cgc tgg atg aaa gcc atg atc cac 288
 Glu Gly Phe Asn Phe Gln Arg Phe Arg Trp Met Lys Ala Met Ile His
 85 90 95

atg atc aag gag att aat aag agg aag gat att ttg ccc aac atc act 336
 Met Ile Lys Glu Ile Asn Lys Arg Lys Asp Ile Leu Pro Asn Ile Thr
 100 105 110

ctg ggc tat cag atc ttt gat acc tgt ttt acc atc tcc aaa tca gtg 384
 Leu Gly Tyr Gln Ile Phe Asp Thr Cys Phe Thr Ile Ser Lys Ser Val
 115 120 125

gaa gca gtc ttg gta ttt ctt aca ggg cag gaa gaa aac agg ccc aat 432
 Glu Ala Val Leu Val Phe Leu Thr Gly Gln Glu Asn Arg Pro Asn
 130 135 140

ttt aga aac agc act gga gca ttt ccg gca gga att gtt gga gca ggt 480
 Phe Arg Asn Ser Thr Gly Ala Phe Pro Ala Gly Ile Val Gly Ala Gly
 145 150 155 160

gga tca ttc tta tca gtt cct gct tca aga att cta ggg tta tat tat 528
 Gly Ser Phe Leu Ser Val Pro Ala Ser Arg Ile Leu Gly Leu Tyr Tyr
 165 170 175

ttg cct cag gtg ggc tat acc tct acc tgc gtg att ctt agt gac aaa 576
 Leu Pro Gln Val Gly Tyr Thr Ser Thr Cys Val Ile Leu Ser Asp Lys
 180 185 190

tac cag ttt cca tct tat ctt cgt gta ata gcc agc gat aag atc cag 624
 Tyr Gln Phe Pro Ser Tyr Leu Arg Val Ile Ala Ser Asp Lys Ile Gln
 195 200 205

tcg aag gct gtg gta aaa cgt atc caa cac ttt 657
 Ser Lys Ala Val Val Lys Arg Ile Gln His Phe
 210 215

<210> 2

<211> 219

<212> PRT

<213> Homo sapiens

<400> 2

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Phe	Leu	Ala	Phe	Leu	Trp	Ala	Glu	Leu	Gly	Ser	Glu	Ala	Lys	Glu	Glu
		20					25					30			
Lys	Glu	Glu	Glu	Arg	Thr	Cys	Arg	Leu	Leu	Gly	Lys	Cys	Val	Asp	Ala
	35					40					45				
Glu	Asn	His	Ser	Leu	Val	Ile	Gly	Gly	Leu	Phe	Pro	Ile	Asp	Ser	Arg
	50					55				60					
Thr	Ile	Pro	Ala	Asn	Glu	Ser	Ile	Leu	Glu	Pro	Ala	Ser	Ala	Lys	Cys
65				70					75					80	
Glu	Gly	Phe	Asn	Phe	Gln	Arg	Phe	Arg	Trp	Met	Lys	Ala	Met	Ile	His
			85				90						95		
Met	Ile	Lys	Glu	Ile	Asn	Lys	Arg	Lys	Asp	Ile	Leu	Pro	Asn	Ile	Thr
		100					105					110			
Leu	Gly	Tyr	Gln	Ile	Phe	Asp	Thr	Cys	Phe	Thr	Ile	Ser	Lys	Ser	Val
	115					120					125				
Glu	Ala	Val	Leu	Val	Phe	Leu	Thr	Gly	Gln	Glu	Glu	Asn	Arg	Pro	Asn
	130					135					140				
Phe	Arg	Asn	Ser	Thr	Gly	Ala	Phe	Pro	Ala	Gly	Ile	Val	Gly	Ala	Gly
145					150				155					160	
Gly	Ser	Phe	Leu	Ser	Val	Pro	Ala	Ser	Arg	Ile	Leu	Gly	Leu	Tyr	Tyr
			165				170						175		
Leu	Pro	Gln	Val	Gly	Tyr	Thr	Ser	Thr	Cys	Val	Ile	Leu	Ser	Asp	Lys
		180					185					190			
Tyr	Gln	Phe	Pro	Ser	Tyr	Leu	Arg	Val	Ile	Ala	Ser	Asp	Lys	Ile	Gln
	195					200					205				
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	210					215									

<210> 3

<211> 657

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:2.

<221> misc_feature

<222> 12, 15, 33, 36, 39, 54, 57, 63, 69, 75, 78, 81, 87, 111,

114, 120, 123, 126, 129, 138, 144, 156, 159, 162, 168, 171,
174, 180, 189, 192, 195, 201, 204, 213, 219, 225, 228, 231,
234, 246, 261, 267, 279, 312, 324, 327, 336, 339, 342
<223> n = A,T,C or G

<221> misc_feature
<222> 360, 369, 375, 381, 384, 390, 393, 396, 399, 405, 408, 411,
426, 429, 438, 444, 447, 450, 453, 459, 462, 465, 471, 474,
477, 480, 483, 486, 492, 495, 498, 501, 504, 507, 510, 516,
519, 522, 531, 534, 540, 543, 549, 552, 555, 561, 567
<223> n = A,T,C or G

<221> misc_feature
<222> 570, 588, 591, 597, 600, 603, 609, 612, 627, 633, 636, 639,
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<223> n = A,T,C or G

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ytntynggna artgygtnga ygcngaraay caywsnytnng tnathggngg nytnnttyccn 180
athgaywsnm gnacnathcc ngcnaaygar wsnathytnng arccngcnws ngcnaartgy 240
garggnttya ayttycarmg nttymgntgg atgaargcna tgathcayat gathaargar 300
athaayaarm gnaargayat hytnccnaay athacnytnng gntaycarat httygayacn 360
tgyttyacna thwsnaarws ngtnngargcn gtntyngntnt tyytnacngg ncargargar 420
aaymgncna ayttymgnaa ywsnacnggn gcnttyccng cnggnathgt nggngcnggn 480
ggwnsnttyy tnwsngtncc ngcnwsnmgn athytnngny tntaytayyt nccncargtn 540
ggntayacnw snacntgygt nathytnwsn gayaartayc arttyccnws ntayytnmgn 600
gtathgcnw sngayaarat hcarwsnaar gcngtngtna armgnathca rcaytty 657

<210> 4
<211> 1140
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1140)

<400> 4
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Leu Pro His Ser Val Cys Thr Asp Val Cys Pro Pro Gly Thr Gly Arg
1 5 10 15

gga ttc gtt cag agg gaa cca ata tgc tgc ttt gac tcc atc cca tgt 96
 Gly Phe Val Gln Arg Glu Pro Ile Cys Cys Phe Asp Ser Ile Pro Cys
 20 25 30

gct gat gga cac gtg tca cgg aaa cca ggt gaa agg gag tgt gaa caa 144
 Ala Asp Gly His Val Ser Arg Lys Pro Gly Glu Arg Glu Cys Glu Gln
 35 40 45

tgt ggt gaa gac tat tgg tca aat gca caa aag agc gag tgt gtg ctg 192
 Cys Gly Glu Asp Tyr Trp Ser Asn Ala Gln Lys Ser Glu Cys Val Leu
 50 55 60

aaa gag gtg gaa tac ctt gct tat gat gag gcc ctg gga ttc aca ctt 240
 Lys Glu Val Glu Tyr Leu Ala Tyr Asp Glu Ala Leu Gly Phe Thr Leu
 65 70 75 80

gtc att ctt tct gtc ttt ggg gca ttt gtg gtc ttg gca gtc aca gct 288
 Val Ile Leu Ser Val Phe Gly Ala Phe Val Val Leu Ala Val Thr Ala
 85 90 95

gtg tat gtg ata cac agg cac act ccc ctg gtg aac gcc agt gac tgg 336
 Val Tyr Val Ile His Arg His Thr Pro Leu Val Asn Ala Ser Asp Trp
 100 105 110

cag ctg ggc ttt ctc att cag gtt tct ctg atc atc atg ctg ctg tct 384
 Gln Leu Gly Phe Leu Ile Gln Val Ser Leu Ile Ile Met Leu Leu Ser
 115 120 125

tcc atg ctt ttc att gac aag cca cac aac tgg tcc tgc atg gct ggc 432
 Ser Met Leu Phe Ile Asp Lys Pro His Asn Trp Ser Cys Met Ala Gly
 130 135 140

cag gtc act ctg gca ctg ggc ttt tct ctt tgc ctg tct tgc ctt ctt 480
 Gln Val Thr Leu Ala Leu Gly Phe Ser Leu Cys Leu Ser Cys Leu Leu
 145 150 155 160

gga aag act agt tca ctg ttt tta gcc tac aga att tcc aaa tcc aaa 528
 Gly Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser Lys Ser Lys
 165 170 175

act caa ctt aca tcc atg cac ccc ctt tat cgg aaa atc att gtg cta 576

TGGTTT "95E000T"

Thr	Gln	Leu	Thr	Ser	Met	His	Pro	Leu	Tyr	Arg	Lys	Ile	Val	Leu	
			180					185					190		
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Ile	Ser	Val	Leu	Ala	Glu	Ile	Gly	Ile	Cys	Thr	Ala	Tyr	Leu	Ile	Leu
		195					200					205			
gaa	cct	ccc	atg	gta	tac	aag	aac	atg	gaa	tct	caa	aat	aca	aag	atc
Glu	Pro	Pro	Met	Val	Tyr	Lys	Asn	Met	Glu	Ser	Gln	Asn	Thr	Lys	Ile
	210					215					220				
att	ctg	gga	tgc	aat	gaa	att	tcc	ata	gag	ttt	ttg	tac	tcg	atg	ttt
Ile	Leu	Gly	Cys	Asn	Glu	Ile	Ser	Ile	Glu	Phe	Leu	Tyr	Ser	Met	Phe
225					230					235					240
gga	att	gat	gcc	ttc	tta	gcc	ttg	cta	tgc	ttt	ctt	aca	act	ttt	gtg
Gly	Ile	Asp	Ala	Phe	Leu	Ala	Leu	Leu	Cys	Phe	Leu	Thr	Thr	Phe	Val
				245					250					255	
gct	cgc	cag	tta	cca	gat	aat	tac	tat	gaa	gga	aaa	tgc	atc	acc	ttt
Ala	Arg	Gln	Leu	Pro	Asp	Asn	Tyr	Tyr	Glu	Gly	Lys	Cys	Ile	Thr	Phe
			260					265					270		
ggg	atg	ctt	gtc	ttt	ttc	atc	att	tgg	atg	tct	ttt	gtc	cct	gtt	tat
Gly	Met	Leu	Val	Phe	Phe	Ile	Ile	Trp	Met	Ser	Phe	Val	Pro	Val	Tyr
		275					280					285			
ttg	agc	acc	aaa	ggc	aag	ttc	aaa	atg	gct	gtg	gaa	ata	ttt	gca	atc
Leu	Ser	Thr	Lys	Gly	Lys	Phe	Lys	Met	Ala	Val	Glu	Ile	Phe	Ala	Ile
		290				295					300				
ttg	gca	tcc	agc	cat	ggc	ttg	ttg	ggt	tgt	ata	ttt	gct	cct	aag	tgc
Leu	Ala	Ser	Ser	His	Gly	Leu	Leu	Gly	Cys	Ile	Phe	Ala	Pro	Lys	Cys
305					310				315						320
ctc	att	att	ttg	ctg	agg	cca	gag	agg	aac	acc	agt	gaa	att	gtt	tgt
Leu	Ile	Ile	Leu	Leu	Arg	Pro	Glu	Arg	Asn	Thr	Ser	Glu	Ile	Val	Cys
				325					330					335	
gga	aga	gtc	tcc	acc	aca	gat	aat	tgc	atc	caa	ctg	acc	tca	gct	ttt
Gly	Arg	Val	Ser	Thr	Thr	Asp	Asn	Cys	Ile	Gln	Leu	Thr	Ser	Ala	Phe
			340					345					350		

gtg agc agt gag ctt aac aat acc aca gtg tca act gtt ctg gat gac 1104
 Val Ser Ser Glu Leu Asn Asn Thr Thr Val Ser Thr Val Leu Asp Asp
 355 360 365

aga gtt ttg att tac atg tgt cct ttg aag ctg caa 1140
 Arg Val Leu Ile Tyr Met Cys Pro Leu Lys Leu Gln
 370 375 380

<210> 5

<211> 380

<212> PRT

<213> Homo sapiens

<400> 5

Leu Pro His Ser Val Cys Thr Asp Val Cys Pro Pro Gly Thr Gly Arg
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 Gly Phe Val Gln Arg Glu Pro Ile Cys Cys Phe Asp Ser Ile Pro Cys
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 Ala Asp Gly His Val Ser Arg Lys Pro Gly Glu Arg Glu Cys Glu Gln
 35 40 45
 Cys Gly Glu Asp Tyr Trp Ser Asn Ala Gln Lys Ser Glu Cys Val Leu
 50 55 60
 Lys Glu Val Glu Tyr Leu Ala Tyr Asp Glu Ala Leu Gly Phe Thr Leu
 65 70 75 80
 Val Ile Leu Ser Val Phe Gly Ala Phe Val Val Leu Ala Val Thr Ala
 85 90 95
 Val Tyr Val Ile His Arg His Thr Pro Leu Val Asn Ala Ser Asp Trp
 100 105 110
 Gln Leu Gly Phe Leu Ile Gln Val Ser Leu Ile Ile Met Leu Leu Ser
 115 120 125
 Ser Met Leu Phe Ile Asp Lys Pro His Asn Trp Ser Cys Met Ala Gly
 130 135 140
 Gln Val Thr Leu Ala Leu Gly Phe Ser Leu Cys Leu Ser Cys Leu Leu
 145 150 155 160
 Gly Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser Lys Ser Lys
 165 170 175
 Thr Gln Leu Thr Ser Met His Pro Leu Tyr Arg Lys Ile Ile Val Leu
 180 185 190
 Ile Ser Val Leu Ala Glu Ile Gly Ile Cys Thr Ala Tyr Leu Ile Leu
 195 200 205
 Glu Pro Pro Met Val Tyr Lys Asn Met Glu Ser Gln Asn Thr Lys Ile
 210 215 220

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Ile Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr Ser Met Phe
225                230                235                240
Gly Ile Asp Ala Phe Leu Ala Leu Leu Cys Phe Leu Thr Thr Phe Val
                245                250                255
Ala Arg Gln Leu Pro Asp Asn Tyr Tyr Glu Gly Lys Cys Ile Thr Phe
                260                265                270
Gly Met Leu Val Phe Phe Ile Ile Trp Met Ser Phe Val Pro Val Tyr
                275                280                285
Leu Ser Thr Lys Gly Lys Phe Lys Met Ala Val Glu Ile Phe Ala Ile
                290                295                300
Leu Ala Ser Ser His Gly Leu Leu Gly Cys Ile Phe Ala Pro Lys Cys
305                310                315                320
Leu Ile Ile Leu Leu Arg Pro Glu Arg Asn Thr Ser Glu Ile Val Cys
                325                330                335
Gly Arg Val Ser Thr Thr Asp Asn Cys Ile Gln Leu Thr Ser Ala Phe
                340                345                350
Val Ser Ser Glu Leu Asn Asn Thr Thr Val Ser Thr Val Leu Asp Asp
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Arg Val Leu Ile Tyr Met Cys Pro Leu Lys Leu Gln
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<210> 6

<211> 1140

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the
amino acid sequence of SEQ ID NO:5.

<221> misc_feature

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69, 87, 93, 99, 105, 111, 114, 117, 123, 126, 132, 150,
165, 171, 180, 189, 192, 201, 210, 213, 225, 228, 231, 237,
240, 243, 249, 252, 255, 261, 264, 270, 273, 276, 279, 282

<223> n = A,T,C or G

<221> misc_feature

<222> 285, 288, 291, 297, 306, 312, 315, 318, 321, 327, 330, 342,
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429, 432, 438, 441, 444, 447, 450, 453, 459, 462, 468, 471,
477, 480, 483, 489, 492, 495, 498, 504, 507, 513, 519

<223> n = A,T,C or G

<221> misc_feature

<222> 525, 531, 537, 540, 543, 552, 555, 561, 573, 576, 582, 585,
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678, 681, 696, 708, 714, 723, 732, 738, 741, 744, 747, 756,
759, 762, 768, 771, 774, 780, 783, 801, 813, 819, 825

<223> n = A,T,C or G

<221> misc_feature

<222> 828, 849, 855, 858, 861, 867, 870, 873, 879, 894, 897, 909,
915, 918, 921, 924, 930, 933, 936, 939, 951, 954, 963, 972,
975, 978, 981, 987, 993, 996, 1005, 1011, 1014, 1017, 1020,
1023, 1026, 1044, 1047, 1050, 1053, 1059, 1062, 1065

<223> n = A,T,C or G

<221> misc_feature

<222> 1071, 1080, 1083, 1086, 1089, 1092, 1095, 1098, 1107, 1110,
1113, 1128, 1131, 1137

<223> n = A,T,C or G

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mgngarccna thtgytgytt ygaywsnath ccntgygcng ayggncaygt nwsnmgnaar 120
ccnggngarm gngartgyga rcartgyggn gargaytayt ggwsnaaygc ncaraarwsn 180
gartgygtny tnaargart ngartayytn gcntaygayg argcnytnng nttyacnytn 240
gtnathytnw sngtnttygg ngcnttygtn gtntngcng tncngcngt ntaygtnath 300
caymgncaya cncnytngt naaygcwnsn gaytggcary tnggnttyt nathcargtn 360
wsnytnatha thatgytnyt nwsnwsnatg ytnttyathg ayaarccnca yaaytggwsn 420
tgyatggcng gncargtnac nytnngcnytn ggnttywsny tntggytnws ntgyytnytn 480
ggnaaracnw snwsnytnntt yytnngcntay mgnathwsna arwsnaarac ncarytnacn 540
wsnatgcayc cnytnntaymg naarathath gtntnytnathw sngtnytngc ngarathggn 600
athtgyacng cntayytnat hytnngarccn ccnatggtnt ayaaraayat ggarwsncar 660
aayacnaara thathytnng ntgyaaygar athwsnathg arttyytna ywsnatgtty 720
ggathgayg cnttyytngc nytnytnytn tyytnacna cnttygtngc nmgnarytn 780
ccngayaayt aytaygargg naartgyath acnttyggna tgytngtntt yttyathath 840
tggatgwsnt tygtncngt ntayytnwsn acnaarggna arttyaarat ggcngtngar 900
athtgyacna thytnngcws nwsncayggn ytnytnngnt gyathhttygc nccnaartgy 960
ytnathathy tnytnmgnc ngarmgnaay acnwsngara thgtntgygg nmngntnwsn 1020
acnacngaya aytgyathca rytnacnwsn gcnttygtntw snwsngaryt naayaayacn 1080
acngtnwsna cngtnytna ygaymgngtn ytnathaya tgtgyccnytn naarytnar 1140

<210> 7

<211> 2781

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric receptor.

<221> CDS

<222> (1)...(2781)

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ttt ctt gca ttt tta tgg gct gaa ttg ggc tct gaa gcc aaa gaa gag	96
Phe Leu Ala Phe Leu Trp Ala Glu Leu Gly Ser Glu Ala Lys Glu Glu	
20 25 30	
aaa gaa gaa gaa cgg acc tgc cgg ttg ctg ggc aag tgt gta gat gcc	144
Lys Glu Glu Glu Arg Thr Cys Arg Leu Leu Gly Lys Cys Val Asp Ala	
35 40 45	
gaa aac cat tcc ctt gtt att gga gga ctg ttt cct att gac tcc agg	192
Glu Asn His Ser Leu Val Ile Gly Gly Leu Phe Pro Ile Asp Ser Arg	
50 55 60	
acc atc cca gca aat gag tct att ttg gag cca gca tca gca aaa tgt	240
Thr Ile Pro Ala Asn Glu Ser Ile Leu Glu Pro Ala Ser Ala Lys Cys	
65 70 75 80	
gaa ggg ttt aac ttt cag aga ttc cgc tgg atg aaa gcc atg atc cac	288
Glu Gly Phe Asn Phe Gln Arg Phe Arg Trp Met Lys Ala Met Ile His	
85 90 95	
atg atc aag gag att aat aag agg aag gat att ttg ccc aac atc act	336
Met Ile Lys Glu Ile Asn Lys Arg Lys Asp Ile Leu Pro Asn Ile Thr	
100 105 110	
ctg ggc tat cag atc ttt gat acc tgt ttt acc atc tcc aaa tca gtg	384
Leu Gly Tyr Gln Ile Phe Asp Thr Cys Phe Thr Ile Ser Lys Ser Val	
115 120 125	
gaa gca gtc ttg gta ttt ctt aca ggg cag gaa gaa aac agg ccc aat	432

Glu	Ala	Val	Leu	Val	Phe	Leu	Thr	Gly	Gln	Glu	Glu	Asn	Arg	Pro	Asn	
130						135				140						
ttt	aga	aac	agc	act	gga	gca	ttt	ccg	gca	gga	att	gtt	gga	gca	ggt	480
Phe	Arg	Asn	Ser	Thr	Gly	Ala	Phe	Pro	Ala	Gly	Ile	Val	Gly	Ala	Gly	
145					150					155					160	
gga	tca	ttc	tta	tca	gtt	cct	gct	tca	aga	att	cta	ggg	tta	tat	tat	528
Gly	Ser	Phe	Leu	Ser	Val	Pro	Ala	Ser	Arg	Ile	Leu	Gly	Leu	Tyr	Tyr	
				165					170					175		
ttg	cct	cag	gtg	ggc	tat	acc	tct	acc	tgc	gtg	att	ctt	agt	gac	aaa	576
Leu	Pro	Gln	Val	Gly	Tyr	Thr	Ser	Thr	Cys	Val	Ile	Leu	Ser	Asp	Lys	
			180					185					190			
tac	cag	ttt	cca	tct	tat	ctt	cgt	gta	ata	gcc	agc	gat	aag	atc	cag	624
Tyr	Gln	Phe	Pro	Ser	Tyr	Leu	Arg	Val	Ile	Ala	Ser	Asp	Lys	Ile	Gln	
		195					200					205				
tcg	aag	gct	gtg	gta	aaa	cgt	atc	caa	cac	ttt	ggg	tgg	gtc	tgg	gta	672
Ser	Lys	Ala	Val	Val	Lys	Arg	Ile	Gln	His	Phe	Gly	Trp	Val	Trp	Val	
	210					215					220					
ggg	gct	att	gca	gct	gat	gat	gat	tat	ggg	aaa	tat	gga	gta	aaa	act	720
Gly	Ala	Ile	Ala	Ala	Asp	Asp	Asp	Tyr	Gly	Lys	Tyr	Gly	Val	Lys	Thr	
225					230					235					240	
ttt	aag	gaa	aaa	atg	gag	agt	gcc	aac	ctc	tgt	gtt	gct	ttc	tct	gaa	768
Phe	Lys	Glu	Lys	Met	Glu	Ser	Ala	Asn	Leu	Cys	Val	Ala	Phe	Ser	Glu	
				245					250					255		
acc	att	ccc	aaa	gtc	tac	tcc	aat	gag	aaa	atg	cag	aag	gct	gtt	aag	816
Thr	Ile	Pro	Lys	Val	Tyr	Ser	Asn	Glu	Lys	Met	Gln	Lys	Ala	Val	Lys	
			260					265					270			
gca	gta	aag	act	tcc	act	gcc	aaa	gtc	att	gtg	ctt	tat	act	tct	gac	864
Ala	Val	Lys	Thr	Ser	Thr	Ala	Lys	Val	Ile	Val	Leu	Tyr	Thr	Ser	Asp	
		275					280					285				
att	gac	ctc	agc	ctg	ttt	gtg	ctg	gaa	atg	att	cat	cat	aac	ata	act	912
Ile	Asp	Leu	Ser	Leu	Phe	Val	Leu	Glu	Met	Ile	His	His	Asn	Ile	Thr	
	290					295					300					

gac Asp 305	agg Arg	aca Thr	tgg Trp	ata Ile	gcc Ala 310	acc Thr	gaa Glu	gcc Ala	tgg Trp	att Ile 315	acc Thr	tct Ser	gct Ala	ctc Leu	att Ile 320	960
gca Ala	aag Lys	cct Pro	gag Glu	tat Tyr 325	ttc Phe	ccc Pro	tat Tyr	ttt Phe	ggg Gly 330	gga Gly	act Thr	att Ile	gga Gly	ttt Phe	gca Ala 335	1008
aca Thr	cca Pro	aga Arg	agt Ser 340	gtt Val	ata Ile	cca Pro	gga Gly	cta Leu 345	aaa Lys	gaa Glu	ttt Phe	ctt Leu	tat Tyr	gat Asp	gta Val 350	1056
cac His	cct Pro	aac Asn 355	aag Lys	gat Asp	cca Pro	aat Asn	gat Asp	gtc Val	ttg Leu	acc Thr	att Ile	gaa Glu	ttc Phe	tgg Trp	caa Gln 360	1104
act Thr 370	gct Ala	ttt Phe	aac Asn	tgt Cys	acc Thr	tgg Trp 375	ccc Pro	aac Asn	agc Ser	agt Ser	gtt Val 380	cct Pro	tat Tyr	aac Asn	gtg Val 385	1152
gat Asp 385	cac His	aga Arg	gtg Val	aat Asn	atg Met 390	act Thr	ggg Gly	aaa Lys	gaa Glu	gac Asp 395	aga Arg	ctg Leu	tat Tyr	gac Asp	atg Met 400	1200
tct Ser	gat Asp	cag Gln	ctc Leu	tgc Cys 405	act Thr	gga Gly	gag Glu	gag Glu	aag Lys 410	ctg Leu	gaa Glu	gat Asp	ctg Leu	aaa Lys	aac Asn 415	1248
acc Thr	tat Tyr	ctg Leu	gat Asp 420	aca Thr	tca Ser	cag Gln	cta Leu	aga Arg	att Ile	aca Thr	aaa Lys	caa Gln	tgt Cys	aaa Lys	caa Gln 425	1296
gct Ala	gta Val	tat Tyr 435	gct Ala	ata Ile	gct Ala	cat His	ggc Gly 440	ctg Leu	gat Asp	cat His	ctc Leu	agc Ser	aga Arg	tgt Cys	caa Gln 445	1344
gaa Glu	ggg Gly	cag Gln	gga Gly	cca Pro	ttt Phe	ggc Gly 455	tca Ser	aat Asn	cag Gln	caa Gln	tgt Cys 460	gca Ala	tat Tyr	ata Ile	cct Pro 465	1392
acc Thr 465	ttt Phe	gat Asp	ttc Phe	tgg Trp	cag Gln 470	cta Leu	atg Met	tac Tyr	tat Tyr	atg Met 475	aaa Lys	gaa Glu	att Ile	aaa Lys	ttt Phe 480	1440

aaa tca cat gag gat aaa tgg gta att ctg gat gat aat gga gat ttg 1488
 Lys Ser His Glu Asp Lys Trp Val Ile Leu Asp Asp Asn Gly Asp Leu
 485 490 495

aaa aat gga cac tat gat gtc cta aac tgg cac tta gat gat gag gga 1536
 Lys Asn Gly His Tyr Asp Val Leu Asn Trp His Leu Asp Asp Glu Gly
 500 505 510

gaa att tcc ttt gtg aca gtt ggg aga ttt aac ttt aga tct aca aac 1584
 Glu Ile Ser Phe Val Thr Val Gly Arg Phe Asn Phe Arg Ser Thr Asn
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ttt gag ctt gtt att cca acg aat tct aca ata ttt tgg aac act gag 1632
 Phe Glu Leu Val Ile Pro Thr Asn Ser Thr Ile Phe Trp Asn Thr Glu
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tca tca agg ctt ccc cat tca gtg tgt act gat gtg tgt cct cct ggg 1680
 Ser Ser Arg Leu Pro His Ser Val Cys Thr Asp Val Cys Pro Pro Gly
 545 550 555 560

act gga agg gga ttc gtt cag agg gaa cca ata tgc tgc ttt gac tcc 1728
 Thr Gly Arg Gly Phe Val Gln Arg Glu Pro Ile Cys Cys Phe Asp Ser
 565 570 575

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 Cys Val Leu Lys Glu Val Glu Tyr Leu Ala Tyr Asp Glu Ala Leu Gly
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ttc aca ctt gtc att ctt tct gtc ttt ggg gca ttt gtg gtc ttg gca 1920
 Phe Thr Leu Val Ile Leu Ser Val Phe Gly Ala Phe Val Val Leu Ala
 625 630 635 640

gtc aca gct gtg tat gtg ata cac agg cac act ccc ctg gtg aac gcc 1968

Val Thr Ala Val Tyr Val Ile His Arg His Thr Pro Leu Val Asn Ala	
645 650 655	
agt gac tgg cag ctg ggc ttt ctc att cag gtt tct ctg atc atc atg	2016
Ser Asp Trp Gln Leu Gly Phe Leu Ile Gln Val Ser Leu Ile Ile Met	
660 665 670	
ctg ctg tcg tcc atg ctt ttc att gac aag cca cac aac tgg tcc tgc	2064
Leu Leu Ser Ser Met Leu Phe Ile Asp Lys Pro His Asn Trp Ser Cys	
675 680 685	
atg gct ggc cag gtc act ctg gca ctg ggc ttt tct ctt tgc ctg tct	2112
Met Ala Gly Gln Val Thr Leu Ala Leu Gly Phe Ser Leu Cys Leu Ser	
690 695 700	
tgc ctt ctt gga aag act agt tca ctg ttt tta gcc tac aga att tcc	2160
Cys Leu Leu Gly Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser	
705 710 715 720	
aaa tcc aaa act caa ctt aca tcc atg cac ccc ctt tat cgg aaa atc	2208
Lys Ser Lys Thr Gln Leu Thr Ser Met His Pro Leu Tyr Arg Lys Ile	
725 730 735	
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Ile Val Leu Ile Ser Val Leu Ala Glu Ile Gly Ile Cys Thr Ala Tyr	
740 745 750	
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Leu Ile Leu Glu Pro Pro Met Val Tyr Lys Asn Met Glu Ser Gln Asn	
755 760 765	
aca aag atc att ctg gga tgc aat gaa att tcc ata gag ttt ttg tac	2352
Thr Lys Ile Ile Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr	
770 775 780	
tcg atg ttt gga att gat gcc ttc tta gcc ttg cta tgc ttt ctt aca	2400
Ser Met Phe Gly Ile Asp Ala Phe Leu Ala Leu Leu Cys Phe Leu Thr	
785 790 795 800	
act ttt gtg gct cgc cag tta cca gat aat tac tat gaa gga aaa tgc	2448
Thr Phe Val Ala Arg Gln Leu Pro Asp Asn Tyr Tyr Glu Gly Lys Cys	
805 810 815	

atc acc ttt ggg atg ctt gtc ttt ttc atc att tgg atg tct ttt gtc 2496
 Ile Thr Phe Gly Met Leu Val Phe Phe Ile Ile Trp Met Ser Phe Val
 820 825 830

cct gtt tat ttg agc acc aaa ggc aag ttc aaa atg gct gtg gaa ata 2544
 Pro Val Tyr Leu Ser Thr Lys Gly Lys Phe Lys Met Ala Val Glu Ile
 835 840 845

ttt gca atc ttg gca tcc agc cat ggc ttg ttg ggt tgt ata ttt gct 2592
 Phe Ala Ile Leu Ala Ser Ser His Gly Leu Leu Gly Cys Ile Phe Ala
 850 855 860

cct aag tgc ctc att att ttg ctg agg cca gag agg aac acc agt gaa 2640
 Pro Lys Cys Leu Ile Ile Leu Leu Arg Pro Glu Arg Asn Thr Ser Glu
 865 870 875 880

att gtt tgt gga aga gtc tcc acc aca gat aat tgc atc caa ctg acc 2688
 Ile Val Cys Gly Arg Val Ser Thr Thr Asp Asn Cys Ile Gln Leu Thr
 885 890 895

tca gct ttt gtg agc agt gag ctt aac aat acc aca gtg tca act gtt 2736
 Ser Ala Phe Val Ser Ser Glu Leu Asn Asn Thr Thr Val Ser Thr Val
 900 905 910

ctg gat gac aga gtt ttg att tac atg tgt cct ttg aag ctg caa 2781
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<213> Artificial Sequence

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			20					25					30		

Lys Glu Glu Glu Arg Thr Cys Arg Leu Leu Gly Lys Cys Val Asp Ala
 35 40 45
 Glu Asn His Ser Leu Val Ile Gly Gly Leu Phe Pro Ile Asp Ser Arg
 50 55 60
 Thr Ile Pro Ala Asn Glu Ser Ile Leu Glu Pro Ala Ser Ala Lys Cys
 65 70 75 80
 Glu Gly Phe Asn Phe Gln Arg Phe Arg Trp Met Lys Ala Met Ile His
 85 90 95
 Met Ile Lys Glu Ile Asn Lys Arg Lys Asp Ile Leu Pro Asn Ile Thr
 100 105 110
 Leu Gly Tyr Gln Ile Phe Asp Thr Cys Phe Thr Ile Ser Lys Ser Val
 115 120 125
 Glu Ala Val Leu Val Phe Leu Thr Gly Gln Glu Glu Asn Arg Pro Asn
 130 135 140
 Phe Arg Asn Ser Thr Gly Ala Phe Pro Ala Gly Ile Val Gly Ala Gly
 145 150 155 160
 Gly Ser Phe Leu Ser Val Pro Ala Ser Arg Ile Leu Gly Leu Tyr Tyr
 165 170 175
 Leu Pro Gln Val Gly Tyr Thr Ser Thr Cys Val Ile Leu Ser Asp Lys
 180 185 190
 Tyr Gln Phe Pro Ser Tyr Leu Arg Val Ile Ala Ser Asp Lys Ile Gln
 195 200 205
 Ser Lys Ala Val Val Lys Arg Ile Gln His Phe Gly Trp Val Trp Val
 210 215 220
 Gly Ala Ile Ala Ala Asp Asp Asp Tyr Gly Lys Tyr Gly Val Lys Thr
 225 230 235 240
 Phe Lys Glu Lys Met Glu Ser Ala Asn Leu Cys Val Ala Phe Ser Glu
 245 250 255
 Thr Ile Pro Lys Val Tyr Ser Asn Glu Lys Met Gln Lys Ala Val Lys
 260 265 270
 Ala Val Lys Thr Ser Thr Ala Lys Val Ile Val Leu Tyr Thr Ser Asp
 275 280 285
 Ile Asp Leu Ser Leu Phe Val Leu Glu Met Ile His His Asn Ile Thr
 290 295 300
 Asp Arg Thr Trp Ile Ala Thr Glu Ala Trp Ile Thr Ser Ala Leu Ile
 305 310 315 320
 Ala Lys Pro Glu Tyr Phe Pro Tyr Phe Gly Gly Thr Ile Gly Phe Ala
 325 330 335
 Thr Pro Arg Ser Val Ile Pro Gly Leu Lys Glu Phe Leu Tyr Asp Val
 340 345 350
 His Pro Asn Lys Asp Pro Asn Asp Val Leu Thr Ile Glu Phe Trp Gln
 355 360 365

Cys Leu Leu Gly Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser
 705 710 715 720
 Lys Ser Lys Thr Gln Leu Thr Ser Met His Pro Leu Tyr Arg Lys Ile
 725 730 735
 Ile Val Leu Ile Ser Val Leu Ala Glu Ile Gly Ile Cys Thr Ala Tyr
 740 745 750
 Leu Ile Leu Glu Pro Pro Met Val Tyr Lys Asn Met Glu Ser Gln Asn
 755 760 765
 Thr Lys Ile Ile Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr
 770 775 780
 Ser Met Phe Gly Ile Asp Ala Phe Leu Ala Leu Leu Cys Phe Leu Thr
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 Thr Phe Val Ala Arg Gln Leu Pro Asp Asn Tyr Tyr Glu Gly Lys Cys
 805 810 815
 Ile Thr Phe Gly Met Leu Val Phe Phe Ile Ile Trp Met Ser Phe Val
 820 825 830
 Pro Val Tyr Leu Ser Thr Lys Gly Lys Phe Lys Met Ala Val Glu Ile
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 Phe Ala Ile Leu Ala Ser Ser His Gly Leu Leu Gly Cys Ile Phe Ala
 850 855 860
 Pro Lys Cys Leu Ile Ile Leu Leu Arg Pro Glu Arg Asn Thr Ser Glu
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 Ile Val Cys Gly Arg Val Ser Thr Thr Asp Asn Cys Ile Gln Leu Thr
 885 890 895
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<221> misc_feature

<222> (1)...(2781)

<223> n = A,T,C or G


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